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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,424A

DATE: 05/09/2002

TIME: 12:54:04

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Output Set: N:\CRF3\05092002\I973424A.raw

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3 <110> APPLICANT: Prayaga, Sudhirdas K
4     Taupier Jr, Raymond J
5     Bandaru, Raj
7 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES HOMOLOGOUS TO THYMOSIN, EPHRIN A
8     RECEPTORS, AND FIBROMODULIN, AND POLYNUCLEOTIDES
9     ENCODING SAME
11 <130> FILE REFERENCE: 15966-585 CIP2
13 <140> CURRENT APPLICATION NUMBER: 09/973,424A
14 <141> CURRENT FILING DATE: 2001-10-09
16 <150> PRIOR APPLICATION NUMBER: 60/159,805
17 <151> PRIOR FILING DATE: 1999-10-15
19 <150> PRIOR APPLICATION NUMBER: 60/159,992
20 <151> PRIOR FILING DATE: 1999-10-18
22 <150> PRIOR APPLICATION NUMBER: 60/160,952
23 <151> PRIOR FILING DATE: 1999-10-22
25 <150> PRIOR APPLICATION NUMBER: 09/689,486
26 <151> PRIOR FILING DATE: 2000-10-12
28 <150> PRIOR APPLICATION NUMBER: 09/687,276
29 <151> PRIOR FILING DATE: 2000-10-13
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33 <170> SOFTWARE: PatentIn Ver. 2.1
35 <210> SEQ ID NO: 1
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37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
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42 <222> LOCATION: (61)..(234)
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47 atg gca gac aaa cca gac ata ggg gaa atc gcc agc ttc aat aag gcc 108
48 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
49 1 5 10 15
51 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag 156
52 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
53 20 25 30
55 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat 204
56 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
57 35 40 45
59 tcc cta ccc ctg tca tct tct aga ccc cag tagtaatgtg gaggaagaat 254
60 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
61 50 55
63 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctgggcactc cgtgctgatg 314

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65 ccaccagcct gaggggtccct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
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79 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
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82 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
83 35 40 45
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86 50 55
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108 cacgggggact ggggctggct caggtatccg gctcatgggt gggactccat caacgaggtg 180
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126 aacctgctgg ccacatgaa ctactccttc tggatcgagg ccgtcaatgg cgtgtccgac 1260
127 ctgagccccg agccccgcgc ggcgctgtgt gtcaacatca ccacgaacca ggcagccccg 1320

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130 gacaaggaga tgcagagcta ctocaccctc aaggccgtca ccaccagagc caccgtctcc 1500
131 ggctcaagc cgggcacccg ctacgtgttc cagggtccgag cccgcacctc agcaggctgt 1560
132 ggccgcttca gccaggccat ggaggtggag accgggaaac cccggccccg ctatgacacc 1620
133 aggaccattg tctggtatct cctgacgtct atcacgggct tgggtgtgct tctgctcctg 1680
134 ctcatctgca agaagaggca ctgtggctac agcaaggcct tccaggactc ggacgaggag 1740
135 aagatgcaact atcagaatgg acaggcaccc ccacctgtct tcctgcctct gcatcacccc 1800
136 ccgggaaagc tcccagagcc ccagttctat gcggaacccc acacctacga ggagccaggc 1860
137 cgggcgggcc gcagtttcac tcgggagatc gaggcctcta ggatccacat cgagaaaatc 1920
138 atcggctctg gtagctccgg ggaagtctgc tacgggagge tgccgggtgcc agggcagcgg 1980
139 gatgtgcccc tggccatcaa ggcctcaaa gccggctaca cggagagaca gaggcgggac 2040
140 ttctgagcgg aggcgtccat catggggcaa ttgcaccatc ccaacatcat ccgcctcgag 2100
141 ggtgtcgtca cccgtggccg cctggcaatg attgtgactg agtacatgga gaacggctct 2160
142 ctggacacct tcctgaggac ccacgacggg cagttcacca tcatgcagct ggtgggcatg 2220
143 ctgagaggag tgggtgccgg catgcgctac ctctcagacc tgggctatgt ccaccgagac 2280
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154 atggtgctac gcatgaacgc ccaggacgtg cgcgccctgg gcatcacct catgggccac 2940
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169           20           25           30
171 Asn Leu Leu Asp Thr Ser Thr Ile His Gly Asp Trp Gly Trp Leu Thr
172           35           40           45
174 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
175           50           55           60
177 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
178           65           70           75           80
180 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
181           85           90           95
183 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
184           100          105          110
186 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu

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264 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
265          530          535          540
267 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu Leu
268 545          550          555          560
270 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
271          565          570          575
273 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
274          580          585          590
276 Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
277          595          600          605
279 Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
280          610          615          620
282 Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
283 625          630          635          640
285 Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
286          645          650          655
288 Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
289          660          665          670
291 Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
292          675          680          685
294 Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
295          690          695          700
297 Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
298 705          710          715          720
300 Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
301          725          730          735
303 Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
304          740          745          750
306 Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
307          755          760          765
309 Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
310          770          775          780
312 Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
313 785          790          795          800
315 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
316          805          810          815
318 Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
319          820          825          830
321 Ala Tyr Gly Glu Arg Pro Tyr Trp Trp Asn Met Thr Asn Arg Asp Val Ile
322          835          840          845
324 Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
325          850          855          860
327 His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
328 865          870          875          880
330 Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
331          885          890          895
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VERIFICATION SUMMARY

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